STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/502,510B*
Source: *IFWP*
Date Processed by STIC: *8/14/06*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
      Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
      prevent "wrapping."

2____Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
      Numbering   use **space characters**, instead.

4____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
      ensure your subsequent submission is saved in ASCII text.**

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
      each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
      residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
      "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
      previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
      the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
      Artificial or Unknown sequences.**

7____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
      (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
      (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
      (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
      This sequence is intentionally skipped
      Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
      (NEW RULES)   <210> sequence id number
      <400> sequence id number
      000

9____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
      (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
      In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
      is Artificial Sequence. (see item 11 below)

11____Use of <220>   Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use
      of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
      Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
      explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
      Sequence Rules

12____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
      "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
      listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

IFWP

RAW SEQUENCE LISTING   DATE: 08/14/2006
PATENT APPLICATION: US/10/502,510B   TIME: 12:24:23

Input Set : E:\04-585SeqListingST25.TXT
Output Set: N:\CRF4\08142006\J502510B.raw

```
 3 <110> APPLICANT: El-Gewely, Mohamed Raafat
 4        El-Gewely, Mohamed Raafat
 5        Gardner, Rebecca
 7 <120> TITLE OF INVENTION: Methods of screening molecular libraries and active
molecules
 8        identified thereby
10 <130> FILE REFERENCE: MBHB-04-585 (59.68.75763/001)
12 <140> CURRENT APPLICATION NUMBER: US/10/502,510B
12 <141> CURRENT FILING DATE: 2004-07-23
12 <150> PRIOR APPLICATION NUMBER: PCT/GB03/00291
13 <151> PRIOR FILING DATE: 2003-01-03
15 <160> NUMBER OF SEQ ID NOS: 51
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 21
21 <212> TYPE: PRT
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: secretion signal peptide
28 <220> FEATURE:
29 <221> NAME/KEY: UNSURE
30 <222> LOCATION: (1)..(21)
31 <223> OTHER INFORMATION: secretion signal peptide
33 <400> SEQUENCE: 1
35 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
36 1               5                  10                  15
39 Gly Ser Thr Gly Asp
40               20
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 49
45 <212> TYPE: PRT
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: transmembrane domain
52 <220> FEATURE:
53 <221> NAME/KEY: UNSURE
54 <222> LOCATION: (1)..(49)
55 <223> OTHER INFORMATION: transmembrane domain
57 <400> SEQUENCE: 2
59 Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
60 1               5                  10                  15
63 Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
64               20                 25                  30
67 Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
```

C--> 12 lines marked with "C-->" annotation

see pp 2, 4, 6

Does Not Comply
Corrected Diskette Needed

```
68          35                    40                    45
71 Arg
75 <210> SEQ ID NO: 3
76 <211> LENGTH: 5
77 <212> TYPE: PRT
78 <213> ORGANISM: Artificial Sequence
80 <220> FEATURE:
81 <223> OTHER INFORMATION: peptide derivative
84 <220> FEATURE:
85 <221> NAME/KEY: VARIANT
86 <222> LOCATION: (1)..(5)
87 <223> OTHER INFORMATION: peptide derivative
89 <400> SEQUENCE: 3
91 Met Gly Trp Cys Thr
92 1               5
95 <210> SEQ ID NO: 4
96 <211> LENGTH: 190
97 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
100 <220> FEATURE:
101 <223> OTHER INFORMATION: vector
104 <220> FEATURE:
105 <221> NAME/KEY: misc_feature
106 <222> LOCATION: (1)..(190)
107 <223> OTHER INFORMATION: vector
109 <220> FEATURE:
110 <221> NAME/KEY: variation
111 <222> LOCATION: (1)..(190)
112 <223> OTHER INFORMATION: n= A, C, G or T in equal molar ratio
114 <220> FEATURE:
115 <221> NAME/KEY: variation
116 <222> LOCATION: (1)..(190)
117 <223> OTHER INFORMATION: k= G or T in equal molar ratio
119 <400> SEQUENCE: 4
120 ttgacgcaaa tgggcggtag gcgtgtacgg tgggaggtct atataagcag agctcgttta    60
122 gtgaaccgtc agatctctag aagctgggta ccagctgcta gcaagcttgc tagcggccgc   120
124 tcgaggccgg caaggccgga tccagacatg ataagataca ttgatgagtt tggacaaacc   180
126 acaactagaa                                                          190
129 <210> SEQ ID NO: 5
130 <211> LENGTH: 70
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: vector
138 <220> FEATURE:
139 <221> NAME/KEY: misc_feature
140 <222> LOCATION: (1)..(70)
141 <223> OTHER INFORMATION: vector
143 <220> FEATURE:
```

[handwritten annotations:] no n's in this sequence

no k's in this sequence

RAW SEQUENCE LISTING   DATE: 08/14/2006
PATENT APPLICATION: US/10/502,510B   TIME: 12:24:23

Input Set : E:\04-585SeqListingST25.TXT
Output Set: N:\CRF4\08142006\J502510B.raw

```
    144 <221> NAME/KEY: variation
    145 <222> LOCATION: (1)..(70)
    146 <223> OTHER INFORMATION: n= A, C, G or T in equal molar ratio
    148 <220> FEATURE:
    149 <221> NAME/KEY: variation
    150 <222> LOCATION: (1)..(70)
    151 <223> OTHER INFORMATION: k= G or T in equal molar ratio
    153 <400> SEQUENCE: 5
W--> 154 aagagctcgg taccaagaag gagtttacat atgggannkn nknnktgata aggatccaag      60
    156 cttgaattca                                                             70
    159 <210> SEQ ID NO: 6
    160 <211> LENGTH: 23
    161 <212> TYPE: DNA
    162 <213> ORGANISM: Artificial Sequence
    164 <220> FEATURE:
    165 <223> OTHER INFORMATION: synthetic sequence
    168 <220> FEATURE:
    169 <221> NAME/KEY: misc_feature
    170 <222> LOCATION: (1)..(23)
    171 <223> OTHER INFORMATION: synthetic sequence
    173 <400> SEQUENCE: 6
    174 aagagctcgg taccaagaag gag                                              23
    177 <210> SEQ ID NO: 7
    178 <211> LENGTH: 25
    179 <212> TYPE: DNA
    180 <213> ORGANISM: Artificial Sequence
    182 <220> FEATURE:
    183 <223> OTHER INFORMATION: synthetic sequence
    186 <220> FEATURE:
    187 <221> NAME/KEY: misc_feature
    188 <222> LOCATION: (1)..(25)
    189 <223> OTHER INFORMATION: synthetic sequence
    191 <400> SEQUENCE: 7
    192 ctgaattcaa gcttggatcc ttatc                                            25
    195 <210> SEQ ID NO: 8
    196 <211> LENGTH: 20
    197 <212> TYPE: DNA
    198 <213> ORGANISM: Artificial Sequence
    200 <220> FEATURE:
    201 <223> OTHER INFORMATION: primer
    204 <220> FEATURE:
    205 <221> NAME/KEY: misc_feature
    206 <222> LOCATION: (1)..(20)
    207 <223> OTHER INFORMATION: primer
    209 <400> SEQUENCE: 8
    210 agagctcgtt tagtgaaccg                                                  20
    213 <210> SEQ ID NO: 9
    214 <211> LENGTH: 20
    215 <212> TYPE: DNA
```

```
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: primer
222 <220> FEATURE:
223 <221> NAME/KEY: misc_feature
224 <222> LOCATION: (1)..(20)
225 <223> OTHER INFORMATION: primer
227 <400> SEQUENCE: 9
228 gtggtttgtc caaactcatc                                        20
231 <210> SEQ ID NO: 10
232 <211> LENGTH: 55
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
236 <220> FEATURE:
237 <223> OTHER INFORMATION: library sequence
240 <220> FEATURE:
241 <221> NAME/KEY: misc_feature
242 <222> LOCATION: (1)..(55)
243 <223> OTHER INFORMATION: library sequence
245 <400> SEQUENCE: 10
246 ggtaccaaga aggagtttac atatgggatg gtgtacttga taaggatcca agctt    55
249 <210> SEQ ID NO: 11
250 <211> LENGTH: 20
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: primer
258 <220> FEATURE:
259 <221> NAME/KEY: misc_feature
260 <222> LOCATION: (1)..(20)
261 <223> OTHER INFORMATION: primer
263 <400> SEQUENCE: 11
264 ctacctcagg cagctcaagc                                        20
267 <210> SEQ ID NO: 12
268 <211> LENGTH: 20
269 <212> TYPE: DNA
270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: primer
276 <220> FEATURE:
277 <221> NAME/KEY: misc_feature
278 <222> LOCATION: (1)..(20)
279 <223> OTHER INFORMATION: primer
281 <400> SEQUENCE: 12
282 agacagcacc ctcatcatgc                                        20
285 <210> SEQ ID NO: 13
286 <211> LENGTH: 20
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial Sequence
```

[Handwritten annotations in right margin: "insufficient explanation - what is the source of the genetic material? (see item 11 on Error Summary Sheet) Please correct these types of errors in subsequent sequences"]

```
290 <220> FEATURE:
291 <223> OTHER INFORMATION: primer
294 <220> FEATURE:
295 <221> NAME/KEY: misc_feature
296 <222> LOCATION: (1)..(20)
297 <223> OTHER INFORMATION: primer
299 <400> SEQUENCE: 13
300 tggtgctcat cttaatggcc                                              20
303 <210> SEQ ID NO: 14
304 <211> LENGTH: 20
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: primer
312 <220> FEATURE:
313 <221> NAME/KEY: misc_feature
314 <222> LOCATION: (1)..(20)
315 <223> OTHER INFORMATION: primer
317 <400> SEQUENCE: 14
318 tgacaaaacc taacttgcgc                                              20
321 <210> SEQ ID NO: 15
322 <211> LENGTH: 26
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: primer
330 <220> FEATURE:
331 <221> NAME/KEY: misc_feature
332 <222> LOCATION: (1)..(26)
333 <223> OTHER INFORMATION: primer
335 <400> SEQUENCE: 15
336 aagcagtggt aacaacgcag agtact                                       26
339 <210> SEQ ID NO: 16
340 <211> LENGTH: 23
341 <212> TYPE: DNA
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: primer
348 <220> FEATURE:
349 <221> NAME/KEY: misc_feature
350 <222> LOCATION: (1)..(23)
351 <223> OTHER INFORMATION: primer
353 <400> SEQUENCE: 16
354 aagcagtggt aacaacgcag agt                                          23
357 <210> SEQ ID NO: 17
358 <211> LENGTH: 34
359 <212> TYPE: DNA
360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/14/2006
PATENT APPLICATION: US/10/502,510B   TIME: 12:24:25

Input Set : E:\04-585SeqListingST25.TXT
Output Set: N:\CRF4\08142006\J502510B.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 37,38,40,41,43,44
Seq#:42; N Pos. 37,38,40,41,43,44
Seq#:51; Xaa Pos. 2

VERIFICATION SUMMARY   DATE: 08/14/2006
PATENT APPLICATION: US/10/502,510B   TIME: 12:24:25

Input Set : **E:\04-585SeqListingST25.TXT**
Output Set: **N:\CRF4\08142006\J502510B.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:1007 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0